

2121

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/990,415
Source: OIP
Date Processed by STIC: 2/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or;
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRE SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

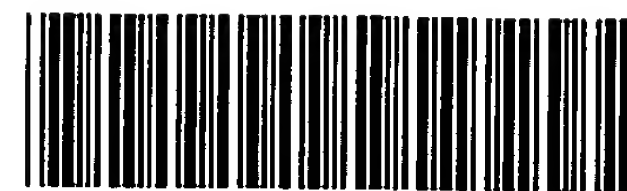
SUGGESTED CORRECTION

SERIAL NUMBER: 09/990,415

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002

TIME: 12:16:35

pg 1-10

Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

3 <110> APPLICANT: Pharmacia AB
 5 <120> TITLE OF INVENTION: Protein Cluster I
 7 <130> FILE REFERENCE: 00349
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/990,415
 C--> 9 <141> CURRENT FILING DATE: 2001-11-21
 9 <160> NUMBER OF SEQ ID NOS: 8
 11 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1232
 15 <212> TYPE: DNA
 16 <213> ORGANISM: human
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (450)..(1232)
 24 <400> SEQUENCE: 1

see item 1 on Error Summary
sheet
 (global
 format error)

E--> 25 cccttaggcg ccagggacag ccgagcgta cctgggtccc ggcagcggag ttctttaccc → 60
 26 60
 E--> 28 accccagttc tggttctgac gccctagctc attccgcaaa tttagggctt gggctctggct → 120
 29 120
 E--> 31 tgttcccctc cggctcgaac cacctcttct ctgagccgag ccagctaccg gggctcctgg
 32 180
 E--> 34 aattgccacc cctccctggg cacccttgag gcctccgtgg agggacgtca cggggcagag
 35 240
 E--> 37 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat
 38 300
 E--> 40 ccccggtgcc accgggtggg cgcggccggg aagctcctgc ccctccctgc tggtcggcgt
 41 360
 E--> 43 cacgcgtgac gtcccgcgtg atggctggga gggcccggcg gcgacagcgg aggcagagag
 44 420
 E--> 46 gaaggcgggt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg
 47 473
 48 Met Glu Ser Lys Met Gly Glu Leu
 49 1 5
 E--> 51 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc
 52 521
 53 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
 54 10 15 20
 E--> 56 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg
 57 569

RAW SEQUENCE LISTING

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Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

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58 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
59 25                      30                      35                      40
E--> 61 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac
62 617
63 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
64                      45                      50                      55
E--> 66 tac agg gcc ggc gtg gtg acc cca ggg atc acc gag gac cag ctg tgg
67 665
68 Tyr Arg Ala Gly Val Val Thr Pro Gly Ile Thr Glu Asp Gln Leu Trp
69                      60                      65                      70
E--> 71 agg gcc aag tat gtg tat gac tcc gcc ttc cat ccg gac aca ggg gag
72 713
73 Arg Ala Lys Tyr Val Tyr Asp Ser Ala Phe His Pro Asp Thr Gly Glu
74                      75                      80                      85
E--> 76 aag gtg gtc ctg att ggc cgc atg tca gcc cag gtg ccc atg aac atg
77 761
78 Lys Val Val Leu Ile Gly Arg Met Ser Ala Gln Val Pro Met Asn Met
79 90                      95                      100
E--> 81 acc atc act ggc tgc atg ctc aca ttc tac agg aag acc cca acc gtg
82 809
83 Thr Ile Thr Gly Cys Met Leu Thr Phe Tyr Arg Lys Thr Pro Thr Val
84 105                      110                      115                      120
E--> 86 gtg ttc tgg cag tgg gtg aat cag tcc ttc aat gcc att gtt aac tac
87 857
88 Val Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Ile Val Asn Tyr
89                      125                      130                      135
E--> 91 tcc aac cgc agt ggt gac act ccc atc act gtg agg cag ctg ggg aca
92 905
93 Ser Asn Arg Ser Gly Asp Thr Pro Ile Thr Val Arg Gln Leu Gly Thr
94                      140                      145                      150
E--> 96 gcc tat gtg agt gcc acc act gga gct gtg gcc acg gcc ctg gga ctc
97 953
98 Ala Tyr Val Ser Ala Thr Thr Gly Ala Val Ala Thr Ala Leu Gly Leu
99                      155                      160                      165
E--> 101 aaa tcc ctc acc aag cac ctg ccc ccc ttg gtc ggc aga ttt gtg ccc
102 1001
103 Lys Ser Leu Thr Lys His Leu Pro Pro Leu Val Gly Arg Phe Val Pro
104 170                      175                      180
E--> 106 ttt gca gca gtg gca gct gcc aac tgc atc aac atc ccc ctg atg agg
107 1049
108 Phe Ala Ala Val Ala Ala Ala Asn Cys Ile Asn Ile Pro Leu Met Arg
109 185                      190                      195                      200
E--> 111 cag aga gag ctg cag gtg ggc atc ccg gtg gct gat gag gca ggt cag
112 1097
113 Gln Arg Glu Leu Gln Val Gly Ile Pro Val Ala Asp Glu Ala Gly Gln
114                      205                      210                      215
E--> 116 agg ctt ggc tac tcg gtg act gca gcc aag cag gga atc ttc cag gtg
117 1145
118 Arg Leu Gly Tyr Ser Val Thr Ala Ala Lys Gln Gly Ile Phe Gln Val

```



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Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

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119          220          225          230
E--> 121 gtg att tca aga atc tgc atg gcg att cct gcc atg gcc atc cca cca
122 1193
123 Val Ile Ser Arg Ile Cys Met Ala Ile Pro Ala Met Ala Ile Pro Pro
124          235          240          245
E--> 126 ctg atc atg gac act ctg gag aag aaa gac ttc ctg aag
127 1232
128 Leu Ile Met Asp Thr Leu Glu Lys Lys Asp Phe Leu Lys
129          250          255          260
190 <210> SEQ ID NO: 3
191 <211> LENGTH: 1061
192 <212> TYPE: DNA
193 <213> ORGANISM: human
195 <220> FEATURE:
196 <221> NAME/KEY: CDS
197 <222> LOCATION: (450)..(680)
199 <400> SEQUENCE: 3
E--> 200 cccttaggcg ccagggacag ccgagcgta cctgggtccc ggcagcggag ttctttaccc
201 60
E--> 203 accccagttc tggttctgac gcctagctc attccgcaaa ttagggctt gggctctggct
204 120
E--> 206 tgttcccctc cggtcgaac cacctcttct ctgagccgag ccagctaccg gggctcctgg
207 180
E--> 209 aattgccacc cctccctggg cacccttgag gcctccgtgg agggacgtca cggggcagag
210 240
E--> 212 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat
213 300
E--> 215 ccccggtccc accgggtggg cgcggccggg aagctcctgc ccctccctgc tggtcggcgt
216 360
E--> 218 cacgcgtgac gtcccgcgtg atggctggga gggcccggcg gcgacagcgg aggcagagag
219 420
E--> 221 gaaggcgggt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg
222 473
223          Met Glu Ser Lys Met Gly Glu Leu
224          1          5
E--> 226 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc
227 521
228 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
229          10          15          20
E--> 231 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg
232 569
233 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
234 25          30          35          40
E--> 236 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac
237 617
238 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
239          45          50          55
E--> 241 tac agg aag acc cca acc gtg gtg ttc tgg cag tgg gtg aat cag tcc
242 665

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      330          70          75          80
E--> 332 gag aag atg aat gtc atc ggg cgc atg tct ttc cag ctt cct ggc ggc
      333 343
      334 Glu Lys Met Asn Val Ile Gly Arg Met Ser Phe Gln Leu Pro Gly Gly
      335      85          90          95
E--> 337 atg atc atc acg ggc ttc atg ctc cag ttc tac agg acg atg ccg gcg
      338 391
      339 Met Ile Ile Thr Gly Phe Met Leu Gln Phe Tyr Arg Thr Met Pro Ala
      340 100          105          110          115
E--> 342 gtg atc ttc tgg cag tgg gtg aac cag tcc ttc aat gcc tta gtc aac
      343 439
      344 Val Ile Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Leu Val Asn
      345      120          125          130
E--> 347 tac acc aac agg aat gcg gct tcc ccc aca tca gtc agg cag atg gcc
      348 487
      349 Tyr Thr Asn Arg Asn Ala Ala Ser Pro Thr Ser Val Arg Gln Met Ala
      350      135          140          145
E--> 352 ctt tcc tac ttc aca gcc aca acc act gct gtg gcc acg gct gtg ggc
      353 535
      354 Leu Ser Tyr Phe Thr Ala Thr Thr Thr Ala Val Ala Thr Ala Val Gly
      355      150          155          160
E--> 357 atg aac atg ttg aca aag aaa gcg ccg ccc ttg gtg ggc cgc tgg gtg
      358 583
      359 Met Asn Met Leu Thr Lys Lys Ala Pro Pro Leu Val Gly Arg Trp Val
      360      165          170          175
E--> 362 ccc ttt gcc gct gtg gct gcg gct aac tgt gtc aat atc ccc atg atg
      363 631
      364 Pro Phe Ala Ala Val Ala Ala Ala Asn Cys Val Asn Ile Pro Met Met
      365 180          185          190          195
E--> 367 cga cag agg gag ctc ata aag gga atc tgc gtg aag gac agg aat gaa
      368 679
      369 Arg Gln Arg Glu Leu Ile Lys Gly Ile Cys Val Lys Asp Arg Asn Glu
      370      200          205          210
E--> 372 aat gag att ggt cat tcc cgg aga gct gcg gcc ata ggc atc acc caa
      373 727
      374 Asn Glu Ile Gly His Ser Arg Arg Ala Ala Ala Ile Gly Ile Thr Gln
      375      215          220          225
E--> 377 gta gtt att tct cgg atc acc atg tca gct cct ggg atg atc ttg ctg
      378 775
      379 Val Val Ile Ser Arg Ile Thr Met Ser Ala Pro Gly Met Ile Leu Leu
      380      230          235          240
E--> 382 cca gtc atc atg gaa agg ctt gag aaa ttg cac ttc atg cag aaa gtc
      383 823
      384 Pro Val Ile Met Glu Arg Leu Glu Lys Leu His Phe Met Gln Lys Val
      385      245          250          255
E--> 387 aag gtc ctg cac gcc cca ttg cag gtc atg ctg agc ggg tgc ttc ctc
      388 871
      389 Lys Val Leu His Ala Pro Leu Gln Val Met Leu Ser Gly Cys Phe Leu
      390 260          265          270          275

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E--> 392 atc ttc atg gtg cca gtg gcg tgt ggg ctt ttc cca cag aaa tgt gaa
 393 919
 394 Ile Phe Met Val Pro Val Ala Cys Gly Leu Phe Pro Gln Lys Cys Glu
 395 280 285 290
 E--> 397 ttg cca gtt tcc tat ctg gaa ccg aag ctc caa gac act atc aag gcc
 398 967
 399 Leu Pro Val Ser Tyr Leu Glu Pro Lys Leu Gln Asp Thr Ile Lys Ala
 400 295 300 305
 E--> 402 aag tat gga gaa ctt gag cct tat gtc tac ttc aat aag ggt ctc taa
 403 1015
 404 Lys Tyr Gly Glu Leu Glu Pro Tyr Val Tyr Phe Asn Lys Gly Leu
 405 310 315 320
 E--> 407 atgccccact tcagcaagga ccagtctatt cccatattca ccagctcctc cttagctacg
 408 1075
 E--> 410 tgcacacttg tgtcctcctt cccctttgcc aacaaggcct gaaggccagg gtagattggg
 411 1135
 E--> 413 ggggtgggaca atgaatgcct catacttaca ccctgggtact ggttgattgg acctcagggg
 414 1195
 E--> 416 aaaaaagtga aaaagggtag caaaggccaa tgtcttctag ctgcttcctc aaccctgtc
 417 1255
 E--> 419 ccctgagaga ccagaagctg aggcctctc agggaggaga catccaagca aatcatttgg
 420 1315
 E--> 422 aaaagttagg aaacctttag gattctggtt ccagccaggg ttgaggaaaa gaccttgat
 423 1375
 E--> 425 caaaaggaag cttctatacc tctttcttct tcgcttcctc ctctcccaag caatggaaac
 426 1435
 E--> 428 ttttaccat gtaattctag ctgaactcag gaaaaagaag ggggaaagga ctctgtcccc
 429 1495
 E--> 431 ttggggctca tcacccttcc acatcctcct cctcgtagcc ccctggtcag gcagcttctt
 432 1555
 E--> 434 tttttttttt tc
 435 1567
 507 <210> SEQ ID NO: 7
 508 <211> LENGTH: 2269
 509 <212> TYPE: DNA
 510 <213> ORGANISM: human
 512 <220> FEATURE:
 513 <221> NAME/KEY: CDS
 514 <222> LOCATION: (125)..(1093)
 516 <220> FEATURE:
 517 <221> NAME/KEY: misc_feature
 518 <222> LOCATION: (25)..(25)
 519 <223> OTHER INFORMATION: n=A,T,G or C
 521 <400> SEQUENCE: 7
 E--> 522 gacgcgctcc ggggacgcgc gaggnccgcg tggcgggaga agcgtttccg gtggcggcgg
 523 60
 E--> 525 aggctgcact gagcgggacc tggcgagcag cgcgggcggc agcccggggg aagcgtccgg
 526 120
 E--> 528 gacc atg tct gga gaa cta cca cca aac att aac atc aag gaa cct cga

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Output Set: N:\CRF3\02212002\I990415.raw

```

529 169
530      Met Ser Gly Glu Leu Pro Pro Asn Ile Asn Ile Lys Glu Pro Arg
531      1          5          10          15
E--> 533 tgg gat caa agc act ttc att gga cga gcc aat cat ttc ttc act gta
534 217
535 Trp Asp Gln Ser Thr Phe Ile Gly Arg Ala Asn His Phe Phe Thr Val
536      20          25          30
E--> 538 act gac ccc agg aac att ctg tta acc aac gaa caa ctc gag agt gcg
539 265
540 Thr Asp Pro Arg Asn Ile Leu Leu Thr Asn Glu Gln Leu Glu Ser Ala
541      35          40          45
E--> 543 aga aaa ata gta cat gat tac agg cag gga att gtt cct cct ggt ctt
544 313
545 Arg Lys Ile Val His Asp Tyr Arg Gln Gly Ile Val Pro Pro Gly Leu
546      50          55          60
E--> 548 aca gaa aat gaa ttg tgg aga gca aag tac atc tat gat tca gct ttt
549 361
550 Thr Glu Asn Glu Leu Trp Arg Ala Lys Tyr Ile Tyr Asp Ser Ala Phe
551      65          70          75
E--> 553 cat cct gac act ggt gag aag atg att ttg ata gga aga atg tca gcc
554 409
555 His Pro Asp Thr Gly Glu Lys Met Ile Leu Ile Gly Arg Met Ser Ala
556 80          85          90          95
E--> 558 cag gtt ccc atg aac atg acc atc aca ggt tgt atg atg acg ttt tac
559 457
560 Gln Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Met Thr Phe Tyr
561      100         105         110
E--> 563 agg act acg ccg gct gtg ctg ttc tgg cag tgg att aac cag tcc ttc
564 505
565 Arg Thr Thr Pro Ala Val Leu Phe Trp Gln Trp Ile Asn Gln Ser Phe
566      115         120         125
E--> 568 aat gcc gtc gtc aat tac acc aac aga agt gga gac gca ccc ctc act
569 553
570 Asn Ala Val Val Asn Tyr Thr Asn Arg Ser Gly Asp Ala Pro Leu Thr
571      130         135         140
E--> 573 gtc aat gag ttg gga aca gct tac gtt tct gca aca act ggt gcc gta
574 601
575 Val Asn Glu Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly Ala Val
576      145         150         155
E--> 578 gca aca gct cta gga ctc aat gca ttg acc aag cat gtc tca cca ctg
579 649
580 Ala Thr Ala Leu Gly Leu Asn Ala Leu Thr Lys His Val Ser Pro Leu
581 160         165         170         175
E--> 583 ata gga cgt ttt gtt ccc ttt gct gcc gta gct gct gct aat tgc att
584 697
585 Ile Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Ala Asn Cys Ile
586      180         185         190
E--> 588 aat att cca tta atg agg caa agg gaa ctc aaa gtt ggc att ccc gtc
589 745

```

same

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Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

```

590 Asn Ile Pro Leu Met Arg Gln Arg Glu Leu Lys Val Gly Ile Pro Val
591          195          200          205
E--> 593 acg gat gag aat ggg aac cgc ttg ggg gag tcg gcg aac gct gcg aaa
594 793
595 Thr Asp Glu Asn Gly Asn Arg Leu Gly Glu Ser Ala Asn Ala Ala Lys
596          210          215          220
E--> 598 caa gcc atc acg caa gtt gtc gtg tcc agg att ctc atg gca gcc cct
599 841
600 Gln Ala Ile Thr Gln Val Val Val Ser Arg Ile Leu Met Ala Ala Pro
601          225          230          235
E--> 603 ggc atg gcc atc cct cca ttc att atg aac act ttg gaa aag aaa gcc
604 889
605 Gly Met Ala Ile Pro Pro Phe Ile Met Asn Thr Leu Glu Lys Lys Ala
606 240          245          250          255
E--> 608 ttt ttg aag agg ttc cca tgg atg agt gca ccc att caa gtt ggg tta
609 937
610 Phe Leu Lys Arg Phe Pro Trp Met Ser Ala Pro Ile Gln Val Gly Leu
611          260          265          270
E--> 613 gtt ggc ttc tgt ttg gtg ttt gct aca ccc ctg tgt tgt gcc ctg ttt
614 985
615 Val Gly Phe Cys Leu Val Phe Ala Thr Pro Leu Cys Cys Ala Leu Phe
616          275          280          285
E--> 618 cct cag aaa agt tcc atg tct gtg aca agc ttg gag gcc gag ttg caa
619 1033
620 Pro Gln Lys Ser Ser Met Ser Val Thr Ser Leu Glu Ala Glu Leu Gln
621          290          295          300
E--> 623 gct aag atc caa gag agc cat cct gaa ttg cga cgc gtg tac ttc aat
624 1081
625 Ala Lys Ile Gln Glu Ser His Pro Glu Leu Arg Arg Val Tyr Phe Asn
626          305          310          315
E--> 628 aag gga ttg taa agcagagagg aaacctctgc agctcattct gccactgcaa
629 1133
630 Lys Gly Leu
631 320
E--> 633 agctggtgta gccatgctgg tgagaaaaat cctgttcaac ctgggttctc ccagttacgg
634 1193
E--> 636 aaacctttta aagatccaca ttagcctttt agaataaagc tgctacttta acagagcacc
637 1253
E--> 639 tggcgtgggc caagtgcctg atactccctt acactgaatc atgttatgat ttatagaaat
640 1313
E--> 642 acctttcctg tagcttttat agtcattggt tttcaaagac gatataccag' ccctcaccca
643 1373
E--> 645 ggttttaaaa aagcactggt aggcatagaa taggtgctca gtatatggtc agtaaatggt
646 1433
E--> 648 ctattgatta tcaatcagtg aaaaaagaaa tctgttttaa atactgaatt ttcattcac
649 1493
E--> 651 tcccattgca aatcaaggag atctcagcag tgaactggga aaatacaaaa gctctgggct
652 1553
E--> 654 aatctataaa aacttacctg aaatattaag ggcagtttgc ttctagtgtg gggattgcgc

```



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002

TIME: 12:16:35

Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

655 1613
E--> 657 tagcccaatg aaggtgatga agcttttgga tttggagggt aaaagctcct tcacaccct
658 1673
E--> 660 tccaaaagtc agtcacagac cactgcaaca tgccttcctt gctggatcat tatatacatt
661 1733
E--> 663 cagattgtga gtggattgcc ttggttgact ttttaatttat tgttttttgt tcttataaag
664 1793
E--> 666 atgataatct taccttgcag ttattgactt tatattcaat tatttacatc aaataatgaa
667 1853
E--> 669 ataactgaaa tgtacaaatg tcaaattttg gaagtatatt caataccaat gctgtatgag
670 1913
E--> 672 tgggctgaat ccagttcatt gttttttttt tggtagaag tgagactaca gttccagcta
673 1973
E--> 675 cctacatgtc ttttcttgtc atccttatag atctctttgg ctttcagaaa gatacagtga
676 2033
E--> 678 taatgtgtgt atgaatcagt cacaatgaat tttacttgaa tattgtatgt tgcattccac
679 2093
E--> 681 ttcatttgaa aataatgaaa ccatgtacca ctgtttacat catctgtagt gatttcata
682 2153
E--> 684 ataatatatt taatatgaca gattatgttt caactctgta gatgtttaac gtcatagaca
685 2213
E--> 687 gtcggccctc tgtatccgtg agctctatat ctgtgaattc aaccaagttt ggatgg
688 2269

see next page for more error

<210> 8
<211> 322
<212> PRT
<213> human

<220>
<221> misc_feature
<222> (25)..(25)
<223> n=A, T, G or C

<400> 8

"n" is only used in a nucleotide sequence.

This sequence is
a peptide sequence

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002

TIME: 12:16:36

Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:200 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:302 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:5
M:254 Repeated in SeqNo=5
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:522 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7